

Reconstructing cell cycle and disease progression using deep learning

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Catalog



Abstract

Introduction

Data and Method

Result and Analysis

Discussion



Abstract



Deep convolutional neural networks combined with nonlinear dimension reduction enable reconstructing biological processes based on raw image data.

In this article , the author demonstrates this by reconstructing the cell cycle of Jurkat cells and disease progression in diabetic retinopathy.

In further analysis of Jurkat cells, we detect and separate a subpopulation of dead cells in an unsupervised manner and, in classifying discrete cell cycle stages, we reach a sixfold reduction in error rate compared to a recent approach based on boosting on image features.

In contrast to previous methods, deep learning based predictions are fast enough for on-the-fly analysis in an imaging flow cytometer.



Introduction



Keywords:

Deep learning (Method of data representation learning , from ANN)

CNN (one of FNN , including (convolutional layer) and (pooling layer))

Boosting (It is a method to improve the **accuracy** of any given learning algorithm)

T-SNE (Unsupervised learning, A method of dimensionality reduction for data)

Jurkat cells (A suspension cell line of acute T cell leukemia)

Flow cytometer

Diabetic retinopathy



Introduction



Background:

A major challenge and opportunity in biology is interpreting the increasing amount of information-rich and high-throughput single-cell data.

Here, we focus on imaging data from **fluorescence microscopy**, in particular from imaging flow cytometry (IFC), which combines the **fluorescence sensitivity** and **high-throughput capabilities** of flow cytometry with single-cell imaging.

Deep learning is therefore capable of processing the dramatic increase in information content—compared to spatially integrated fluorescence intensity measurements as in conventional flow cytometry—in IFC data



Introduction



Background:

While this is possible for cell cycle when carrying out elaborate experiments where such markers are measured, in many other cases, this is too tedious, has severe side effects with unwanted influences on the phenomenon itself or is simply not possible as markers for a specific phenomenon are not known

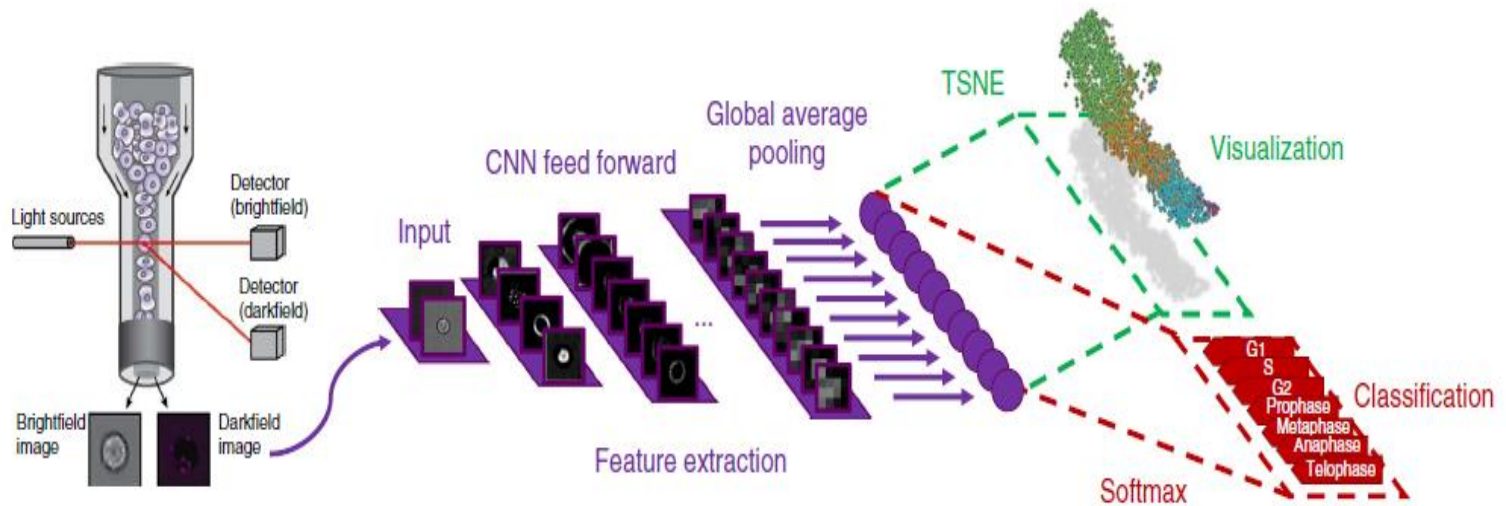
Therefore, we propose a general workflow that uses a deep convolutional neural network combined with classification and visualization based on nonlinear dimension reduction



Introduction



Background:



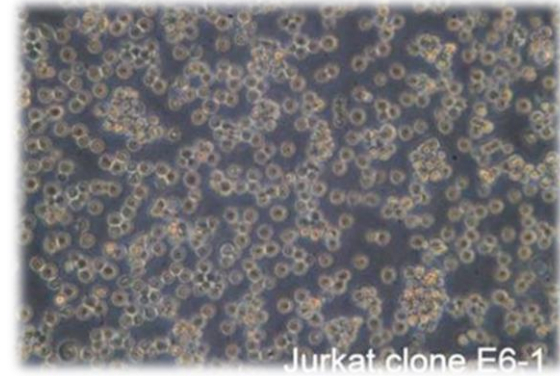


Data and Method



Data

From 32,266 Jurkat cells



Method

PI (碘化丙啶)

MPM2 (有丝分裂蛋白单克隆#2)

DeepFlow



Result and Analysis

1. Reconstructing cell cycle progression

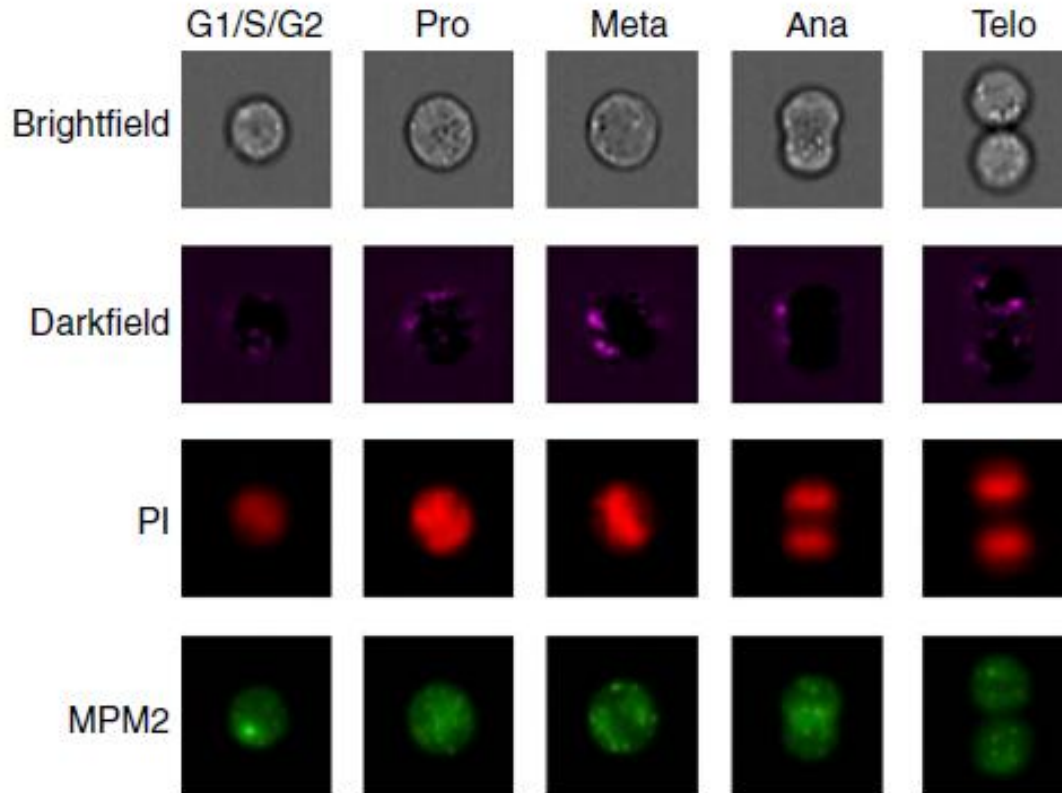
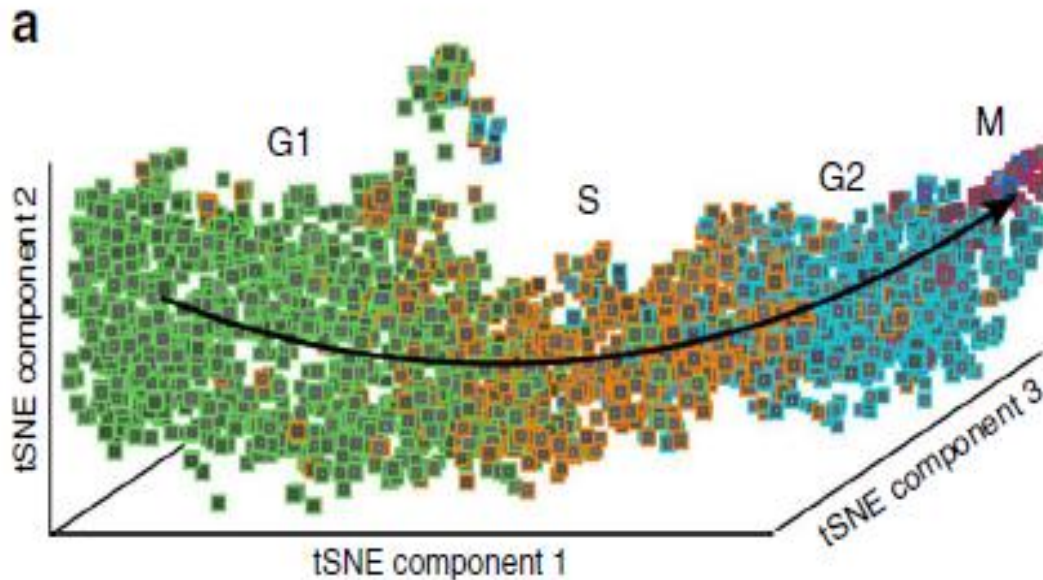


Fig. 2 Representative images for the cell cycle stages as measured in brightfield, darkfield, and fluorescence channels. Seven cell cycle stages define seven classes. We only show one representative image for the interphase classes G1, S, and G2, which can hardly be distinguished by eye



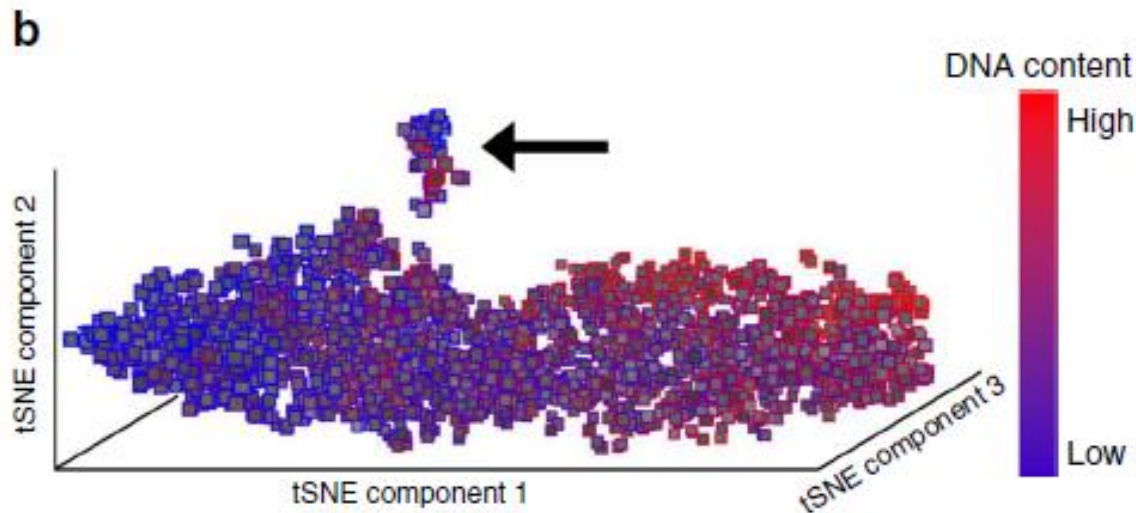
Result and Analysis



We observe that the Jurkat cell data is organized in a long stretched cylinder along which cell cycle phases are ordered in the chronologically correct order



Result and Analysis



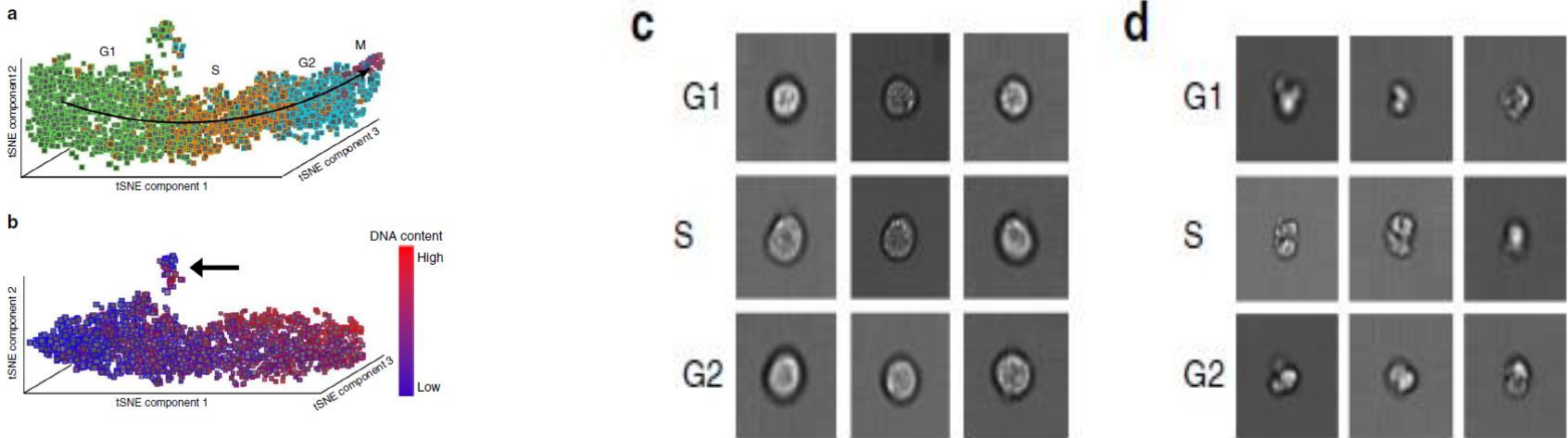
We separately visualized just those cells annotated as being in the interphase classes (G1, S, G2) and colored them with the DNA content obtained from one of the fluorescent channels of the IFC.

The DNA content reflects the continuous progression of cells in G1, S, and G2 on a more fine-grained level. Its correspondence with the longitudinal direction of the cylinder found by tSNE demonstrates that the temporal order learned by the neural network is accurate even beyond the categorical class labels.



Result and Analysis

2. Detecting abnormal cells in an unsupervised manner

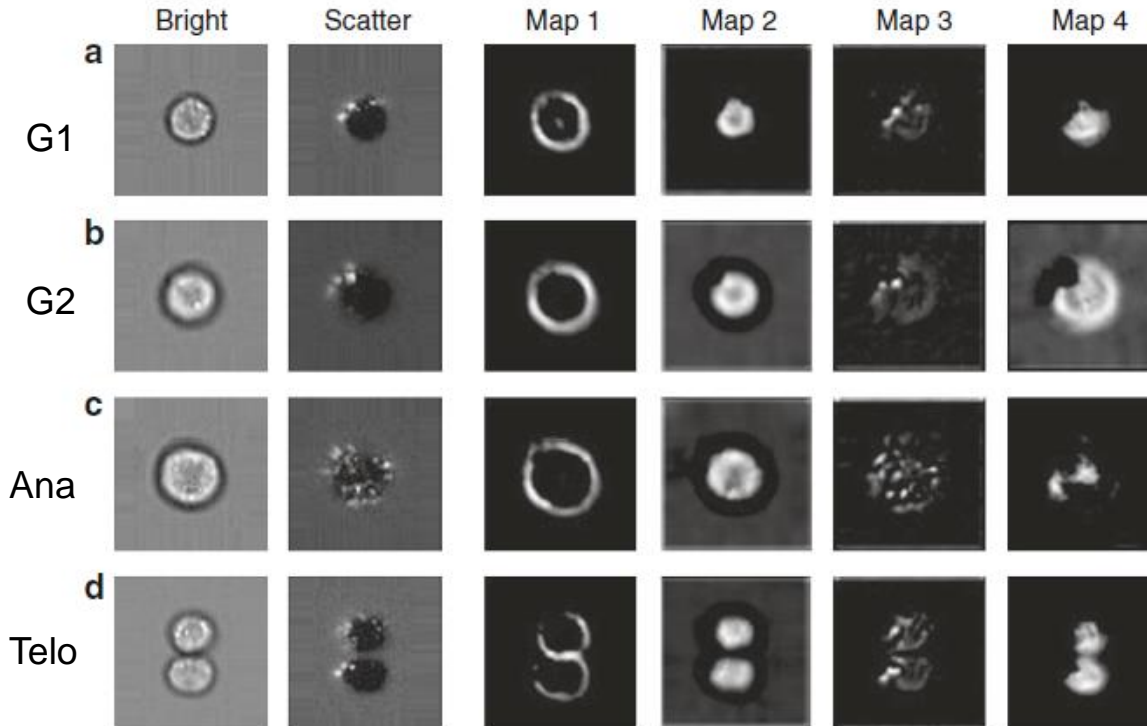


It contains cells from all three interphase classes. While cells in the bulk have high circularity and well defined borders (Fig. 3c) cells in the small cluster are characterized by morphological abnormalities such as broken cell walls and outgrowths, signifying dead cells (Fig. 3d).



Result and Analysis

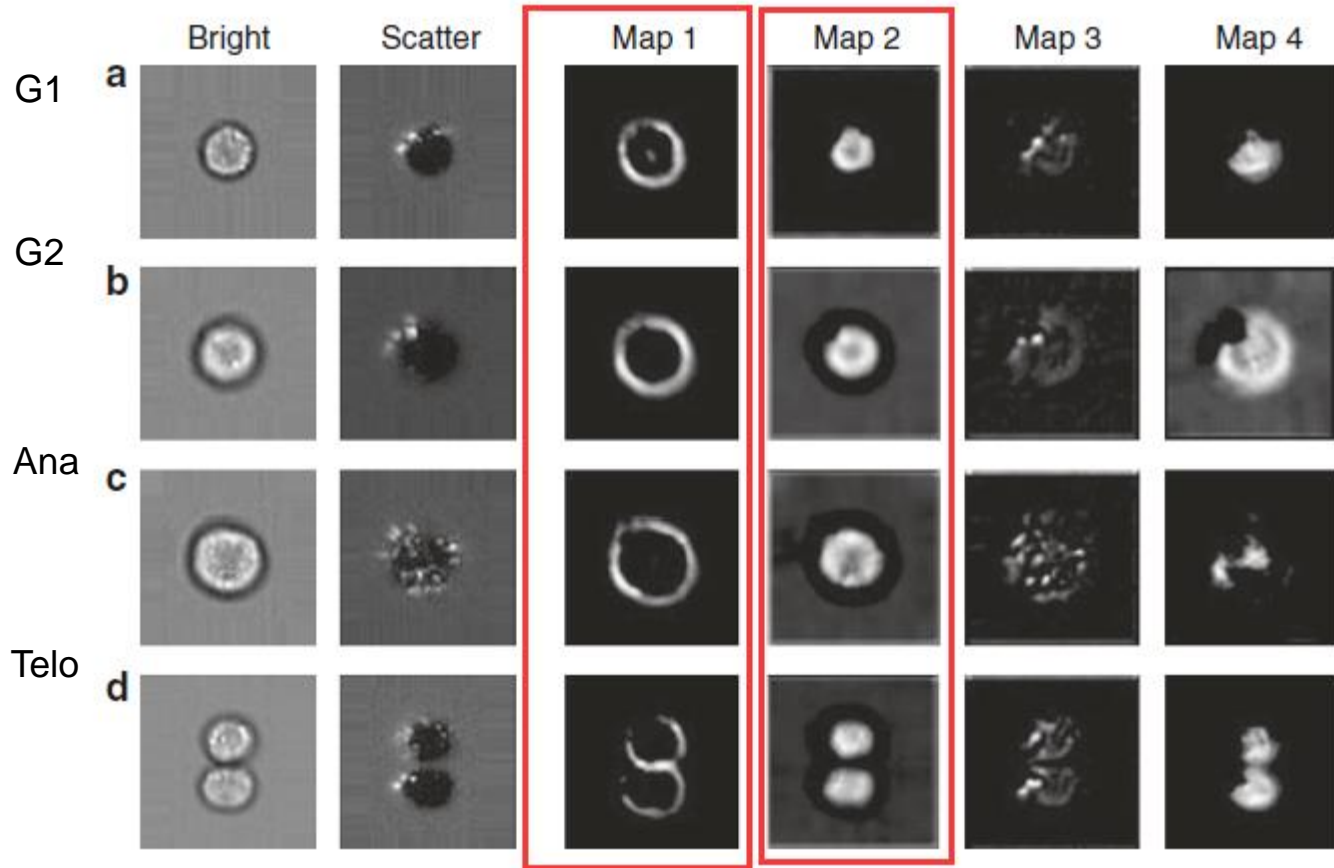
3. Deep learning automatically performs segmentation



We interpret the data representation encoded in one of the trained intermediate layers of the neural network by inspecting its activation patterns using exemplary input data from several classes



Result and Analysis

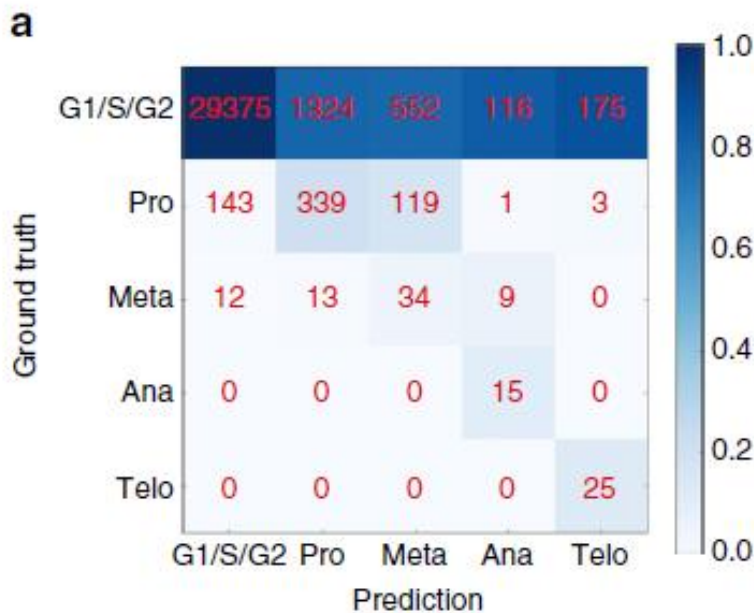


We observe a strong response to features that arise from the cell border thickness (Fig. 4, map 1), to area-based features (Fig. 4, map 2), as well as cross-channel features.

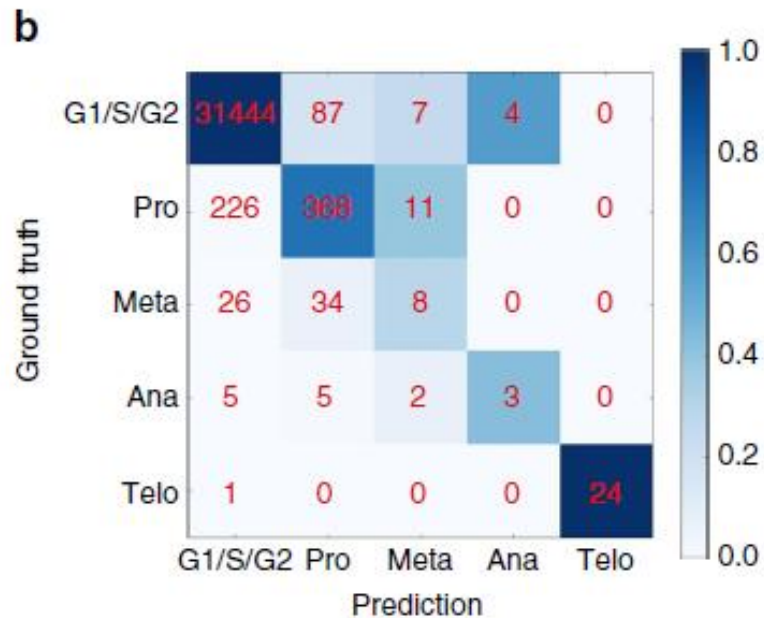


Result and Analysis

4. Deep learning outperforms boosting for cell classification



Boosting : 92.53%

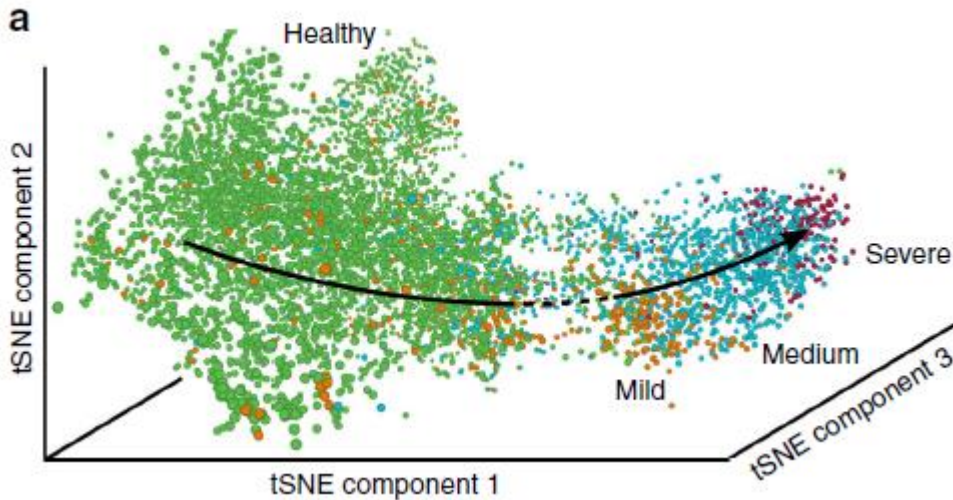


Deep Learning: 98.73% ± 0.16%



Result and Analysis

5. Reconstructing disease progression



30,000 color fundus
photographies of the human
retina

We observe a reconstructed disease progression (Fig. 6) for 8000 samples in the validation data set, that is, the four disease states are ordered along disease severity, even though the network has not been provided with the ordering information.



Discussion



Given the compelling performance on reconstructing the cell cycle and diabetic retinopathy, we expect deep learning to be helpful for understanding **a wide variety of biological processes** involving continuous morphology changes.

Examples include developmental stages of organisms, dose response and the progression of healthy states to disease states, situations that have often been non-ideally reduced to binary classification problems

Our results indicate that reconstructing biological processes is possible for a wide variety of image data, if enough samples are available.



Bright spot

Only one of the other recent works on deep learning in high-throughput microscopy discusses the **visualization of network features**, but none deal with continuous biological processes

Inspiration

In scientific research, we must learn to learn from the crowd, the theory and technology to be integrated

Deficiencies

The direction of disease progression is not universal, only one

The process of cell cycle is not more refined



Thanks for your attention